SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: ARATHOON, R.
                CARTER, P.J.
                MERCHANT, A.M.
                PRESTA, L.G.

   (ii) TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
                       HAVING HETEROMULTIMERIC AND COMMON
                       COMPONENTS

   (iii) NUMBER OF SEQUENCES: 28

   (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: Genentech, Inc.
       (B) STREET: 1 DNA Way
       (C) CITY: South San Francisco
       (D) STATE: California
       (E) COUNTRY: USA
       (F) ZIP: 94080

   (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: WinPatin (Genentech)

   (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER:
       (B) FILING DATE: 07-Mar-2000
       (C) CLASSIFICATION:

   (vii) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: 09/070,418
       (B) FILING DATE: 30-APR-1998

   (viii) ATTORNEY/AGENT INFORMATION:
       (A) NAME: Conley, Deirdre L.
       (B) REGISTRATION NUMBER: 36,487
       (C) REFERENCE/DOCKET NUMBER: P1099R2C1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTTCCCGA GATGGGGGCA GGGTGCACAC CTGTGG 36

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCTTCCCGA CATGGGGGCA G 21

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTCATCTCA CACCGGGATG G 21

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTGGTCATA CATTCACGGG ATGG 24

(2) INFORMATION FOR SEQ ID NO:5:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCTTCCCGA GATGGGGGAC AGGTGTACAC 30

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCCGTCGGAA CACAGCACGG G 21

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 39 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGGAGTCT AGAACGGGAG GCGTGGTACA GTAGTTGTT 39

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCGGAGTCT AGAACGGGAG GACAGGTCTT GTA 33

(2) INFORMATION FOR SEQ ID NO:9:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGGAGTCT AGACAGGGAG G 21

(2) INFORMATION FOR SEQ ID NO:10:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 21 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCGTCGGAG CTCAGCACGG G 21

(2) INFORMATION FOR SEQ ID NO:11:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 24 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGAGGCGTG GTGCTGTAGT TGTT 24

(2) INFORMATION FOR SEQ ID NO:12:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 38 base pairs
       (B) TYPE: Nucleic Acid
       (C) STRANDEDNESS: Single
       (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTCAGGTGC TGGGCTCGGT GGGCTTGTGT GAGTTTTG 38

(2) INFORMATION FOR SEQ ID NO:13:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACGCGTACG CTCTGAAAAT GGCGGACCCG AACCGTTTTC GTGGTAAAGA 50

TCTGGCTGCA CACTACGGCC AGCCGCGGGA ACCTCAGGTG TATACCCTGC 100

CACCGTCTCG AGAAGAAATG ACTAAAAACC AGGTCTCTCT GTGGTGCCTG 150

GTCAAAGGTT TCTATCCGAG CGATATCGCC GTGGAATGGG AAAGCAACGG 200

TCAACCGGAA AACAACTACA AAACCACTCC ACCGGTGCTG GATTCTGATG 250

GCTCCTTCTT TCTGTATTCG AAGCTGACCG TTGACAAAAG CCGTTGGCAG 300

CAAGGCAACG TTTTCAGCTG TTCTGTTATG CACGAGGCCT TGCACAACCA 350

CTACACCCAG AAAAGCCTGT CCCTGTCTCC CGGGAAATAA GCTGAGGCTC 400

CTCTAGAGGT TGAGGTGATT TTATGAAAAA GAATATCGCA TTTCTTCTTG 450

CATCTATGTT CGTTTTTTCT ATTGCTACAA ACGCGTACGC TGGGCAGCCC 500

CGAGAACCAC AGGTGTACAC CCTGCCCCCA TCCCGGGAAG AGATGACCAA 550

GAACCAGGTA AGCTTGTACT GCCTGGTCAA AGGCTTCTAT CCCAGCGACA 600

TCGCCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC 650

ACGCCTCCCG TGCTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCTTTCT 700

CACCGTCGAC AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG 750

TGATGCATGA GGCTCTGCAC AACCACTACA CGCAGAAGAG CCTCTCCCTG 800

TCTCCGGGTA AATAGGGGCC C 811

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Leu Thr Val Leu
                50

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
 1   5   10   15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
                20   25   30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
                35   40   45

Lys Leu Thr Val Leu
                50

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
 1   5   10   15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
                20   25   30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
                35   40   45

Lys Leu Thr Val Leu
                50

(2) INFORMATION FOR SEQ ID NO:17:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
1               5                   10                  15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
                20                  25                  30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
                35                  40                  45

Lys Leu Thr Val Leu
                50
```

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
1               5                   10                  15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
                20                  25                  30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
                35                  40                  45

Lys Leu Thr Val Leu
                50
```

(3) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Ser Thr Ala Ser Leu
```

Lys Leu Thr Val Leu
              50

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Asn Arg Phe Ser Gly Ser Lys Xaa Gly Asn Thr Ala Ser Leu
 1   5   10   15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
                20   25   30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
                35   40   45

Lys Leu Thr Val Leu
              50

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
 1   5   10   15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
                20   25   30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
                35   40   45

Lys Leu Thr Val Leu
              50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
1   5   10   15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
                    20   25   30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
                    35   40   45

Lys Leu Thr Val Leu
                    50

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 62 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
1   5   10   15

Lys Asn Thr Leu Tyr Leu Gln Met Asn Arg Leu Arg Ala Glu Asp
                    20   25   30

Thr Ala Val Tyr Tyr Cys Ala Arg Asp Asn Gly Trp Glu Leu Thr
                    35   40   45

Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Met Val Thr Val
                    50   55   60

Ser Ser
    62

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 62 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Thr Ala Val Tyr Tyr Cys Ala Arg Val Asp Leu Glu Asp Tyr Gly
              35   40   45

Ser Gly Ala Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
              50   55   60

Ser Ser
    62

(2) INFORMATION FOR SEQ ID NO:25:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 107 amino acids
          (B) TYPE: Amino Acid
          (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile
 1   5   10   15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr
              20   25   30

His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
              35   40   45

Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser
              50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
              65   70   75

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
              80   85   90

Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu
              95   100   105

Ile Lys
   107

(2) INFORMATION FOR SEQ ID NO:26:

     (i) SEQUENCE CHARACTERISTICS:

Asn Ala Tyr Ala Leu Lys Met Ala Arg Trp Asn Arg Ile Arg Gly

Lys Asp Leu Ala Ala His Tyr Gly Gln Pro Arg Glu Pro Gln Val
                    20   25   30

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
                    35   40   45

Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
                    50   55   60

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                    65   70   75

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
                    80   85   90

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
                    95   100   105

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
                    110   115   120

Lys Ser Leu Ser Leu Ser Pro Gly Lys Xaa Met Lys Lys Asn Ile
                    125   130   135

Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr Asn
                    140   145   150

Ala Tyr Ala Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
                    155   160   165

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Tyr Cys
                    170   175   180

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                    185   190   195

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                    200   205   210

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Phe Leu Thr Val
                    215   220   225

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                    230   235   240

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 717 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
CAGGTGCAGC TGGTGCAGTC TGGGGGAGGC TTGGTCCGGC CCGGGGGGTC 50

CCTGAGTCTC TCCTGTGCAG TCTCTGGAAT CACCCTCAGG ACCTACGGCA 100

TGCACTGGGT CCGCCAGGCT CCAGGCAAGG GGCTGGAGTG GGTGGCAGGT 150

ATATCCTTTG ACGGAAGAAG TGAATACTAT GCAGACTCCG TGCAGGGCCG 200

ATTCACCATC TCCAGAGACA GTTCCAAGAA CACCCTGTAT CTGCAAATGA 250

ACAGCCTGAG AGCCGAGGAC ACGGCTGTGT ATTACTGTGC GAGAGGAGCA 300

CATTATGGTT CGATATCTG GGGCCAAGGG ACAATGGTCA CCGTCTCGAG 350

TGGTGGAGGC GGTACAGGCG GAGGTGGCAG CGGCGGTGGC GGATCGGACA 400

TCCAGATGAC CCAGTCTCCT TCCACCCTGT CTGCATCTAT TGGAGACAGA 450

GTCACCATCA CCTGCCGGGC CAGCGAGGGT ATTTATCACT GGTTGGCCTG 500

GTATCAGCAG AAGCCAGGGA AAGCCCCTAA ACTCCTGATC TATAAGGCCT 550

CTAGTTTAGC CAGTGGGGCC CCATCAAGGT TCAGCGGCAG TGGATCTGGG 600

ACAGATTTCA CTCTCACCAT CAGCAGCCTG CAGCCTGATG ATTTTGCAAC 650

TTATTACTGC CAACAATATA GTAATTATCC GCTCACTTTC GGCGGAGGGA 700

CCAAGCTGGA GATCAAA 717
```

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 732 base pairs
        (B) TYPE: Nucleic Acid

```
CCTGAGACTC TCCTGTGCAG CCTCTGGATT CACCTTCAGT AGTTATGAAA 100

TGAACTGGGT CCGCCAGGCT CCAGGGAAGG GGCTGGAGTG GGTCTCAGGT 150

ATTAGTGGTA GTGGTGGTAG CACATACTAC GCAGACTCCG TGAAGGGCCG 200

GTTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT CTGCAAATGA 250

ACAGACTGAG AGCTGAGGAC ACGGCTGTGT ATTACTGTGC GAGAGATAAT 300

GGGTGGGAAC TAACGGACTG GTACTTCGAT CTCTGGGGCC GGGGACAAT 350

GGTCACCGTC TCCTCAGGTG GAGGCGGTTC AGGCGGAGGT GGCAGCGGCG 400

GTGGCGGATC GGACATCCAG ATGACCCAGT CTCCTTCCAC CCTGTCTGCA 450

TCTATTGGAG ACAGAGTCAC CATCACCTGC CGGGCCAGTG AGGGTATTTA 500

TCACTGGTTG GCCTGGTATC AGCAGAAGCC AGGGAAAGCC CCTAAACTCC 550

TGATCTATAA GGCCTCTAGT TTAGCCAGTG GGGCCCCATC AAGGTTCAGC 600

GGCAGTGGAT CTGGGACAGA TTTCACTCTC ACCATCAGCA GCCTGCAGCC 650

TGATGATTTT GCAACTTATT ACTGCCAACA ATATAGTAAT TATCCGCTCA 700

CTTTCGGCGG AGGGACCAAG CTGGAGATCA AA 732
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